

Supplementary Table 1 (Page 1 of 5)

Illumina Probeset ID	GeneTitle	Gene Symbol	RIM p-value	RIM q-value	All MDD Subjects (alr)	WM/GM Fold change	Enrichment
ILMN_1812824	Somatostatin	SST	4.09E-05	0.020	-0.84	-1.96	Neuronal
ILMN_1765966	Chromogranin B (secretogranin 1)	CHGB	7.95E-04	0.034	-0.54	-3.76	
ILMN_1679984	Zinc finger, CCHC domain containing 12	ZCCHC12	1.64E-04	0.024	-0.53	-4.24	
ILMN_1697512	Solute carrier family 32 (GABA vesicular transporter), member 1	SLC32A1	4.91E-04	0.030	-0.48	-7.27	
ILMN_1685834	Amphiphysin, transcript variant 1	AMPH	1.63E-03	0.044	-0.39	-2.12	
ILMN_2384409	Tachykinin, precursor 1, transcript variant alpha,	TAC1	2.19E-03	0.048	-0.38	-1.50	
ILMN_1810604	ELMO/CED-12 domain containing 1	ELMOD1	2.17E-03	0.048	-0.38	-2.72	
ILMN_1705153	Neurofilament, heavy polypeptide	NEFH	6.34E-05	0.020	-0.36	-2.14	
ILMN_2354547	Tumor suppressor candidate 3, transcript variant 1	TUSC3	9.76E-04	0.036	-0.34	-1.89	
ILMN_1806147	Guanine nucleotide binding protein (G protein), gamma 3	GNG3	1.35E-04	0.023	-0.31	-1.91	
ILMN_1654632	Regulator of G-protein signaling 7 binding protein	RGS7BP	2.30E-03	0.049	-0.31	-5.46	
ILMN_2043809	Phosphofructokinase, muscle	PFKM	1.13E-04	0.021	-0.31	-1.73	
ILMN_1740265	Acyl-CoA thioesterase 7, transcript variant hBACHb	ACOT7	1.08E-04	0.021	-0.30	-2.10	
ILMN_1673769	Potassium voltage-gated channel, subfamily G, member 1	KCNG1	1.37E-03	0.041	-0.30	-2.17	
ILMN_1751016	LON peptidase N-terminal domain and ring finger 2	LONRF2	1.40E-03	0.041	-0.29	-2.57	
ILMN_1673998	Somatostatin receptor 1	SSTR1	1.34E-03	0.041	-0.28	-2.10	
ILMN_1661622	TBC1 domain family, member 7	TBC1D7	9.63E-04	0.036	-0.28	-1.99	
ILMN_1663092	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain,	CITED2	1.98E-03	0.047	-0.27	-1.70	
ILMN_1695731	Tubulin, gamma 1	TUBG1	5.40E-04	0.031	-0.27	-1.66	
ILMN_1705991	Glucuronidase, beta-like 1	GUSBL1	2.35E-03	0.049	0.28	-1.72	
ILMN_1713301	DiGeorge syndrome critical region gene 2	DGCR2	2.71E-04	0.027	0.28	-1.61	
ILMN_1736154	ProSAPI1 protein	ProSAPI1	6.97E-04	0.033	0.31	-2.60	
ILMN_1760798	Ryanodine receptor 2 (cardiac)	RYR2	7.82E-04	0.034	0.40	-2.65	

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ILMN_2071186	Cortistatin	CORT	1.72E-04	0.025	-0.58	-1.06	Neuronal / Glial
ILMN_1731062	Neuropeptide Y	NPY	3.70E-04	0.029	-0.52	-1.18	
ILMN_1729165	Transcription elongation factor A (SII)-like 6	TCEAL6	8.23E-04	0.035	-0.40	1.41	
ILMN_1771286	PREDICTED: similar to phosphodiesterase 4D interacting protein isoform 2	LOC653513	3.22E-04	0.028	-0.39	1.17	
ILMN_1690397	Dynein, cytoplasmic 1, intermediate chain 1	DYNC111	1.02E-03	0.037	-0.35	-1.20	
ILMN_1704477	cytochrome c oxidase subunit Va	COX5A	2.00E-05	0.018	-0.34	-1.07	
ILMN_1711516	ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A	ATP6V1A	6.44E-04	0.032	-0.33	-1.30	
ILMN_2413084	heat shock 70kDa protein 8, transcript variant 2	HSPA8	7.47E-04	0.034	-0.32	1.01	
ILMN_1659659	melanoma antigen family H, 1	MAGEH1	9.39E-04	0.036	-0.31	1.11	
ILMN_2179018	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1,	NDUFAB1	5.69E-04	0.032	-0.30	-1.47	
ILMN_1757384	RAN, member RAS oncogene family	RAN	1.24E-03	0.040	-0.30	-1.25	
ILMN_1667050	Phosphoribosyl pyrophosphate synthetase 1	PRPS1	2.12E-03	0.048	-0.30	1.02	
ILMN_2179726	Hypothetical protein LOC90835	LOC90835	9.74E-05	0.020	-0.30	-1.27	
ILMN_1686367	Heat shock 70kDa protein 8, transcript variant 1,	HSPA8	1.86E-03	0.046	-0.29	1.02	
ILMN_1759097	Myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila) 11	MLLT11	5.65E-04	0.032	-0.28	-1.29	
ILMN_1694274	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown 2	NDUFC2	1.47E-04	0.024	-0.28	-1.11	
ILMN_1708672	Acetyl-Coenzyme A acetyltransferase 2	ACAT2	8.14E-04	0.034	-0.27	-1.10	
ILMN_1669410	Chromogranin A	CHGA	4.51E-04	0.030	-0.27	1.13	
ILMN_2345015	Prostaglandin E synthase 2 transcript variant 2	PTGES2	1.10E-04	0.021	-0.27	-1.49	
ILMN_1700955	Tctex1 domain containing 2	TCTEX1D2	5.48E-04	0.031	-0.27	1.30	
ILMN_1810759	Chromosome 2 open reading frame 25	C2orf25	3.42E-04	0.029	-0.27	-1.20	
ILMN_2341363	ATP synthase, alpha subunit 1, transcript variant 2,	ATP5A1	4.76E-04	0.030	-0.26	-1.29	
ILMN_1704571	Family with sequence similarity 53, member B	FAM53B	5.08E-04	0.030	0.26	1.42	
ILMN_2368617	Fukutin related protein, transcript variant 1,	FKRP	1.75E-03	0.046	0.26	-1.12	
ILMN_1796216	Vasohibin 1	VASH1	1.28E-04	0.022	0.27	1.49	
ILMN_2152581	Serine/threonine kinase	STK38	6.21E-04	0.032	0.27	-1.49	
ILMN_1737644	Hypothetical protein BC017488, transcript variant 1	LOC124446	4.62E-04	0.030	0.28	1.13	

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Illumina Probeset ID	GeneTitle	Gene Symbol	RIM p-value	RIM q-value	All MDD Subjects (alr)	WM/GM Fold change	Enrichment
ILMN_1692145	Zinc finger protein 14	ZNF14	2.40E-03	0.050	0.28	-1.22	Neuronal / Glial
ILMN_2347193	Gasdermin-like, transcript variant 2	GSDML	7.79E-04	0.034	0.28	-1.08	
ILMN_1658472	Anterior pharynx defective 1 homolog A (C. elegans)	APH1A	8.42E-05	0.020	0.28	1.22	
ILMN_1703330	Fem-1 homolog c (C. elegans)	FEM1C	2.40E-04	0.027	0.28	-1.30	
ILMN_1734483	BSD domain containing 1	BSDC1	4.82E-04	0.030	0.28	-1.21	
ILMN_1796663	beta-1,4-N-acetyl-galactosaminyl transferase 4	B4GALNT4	1.85E-03	0.046	0.29	-1.14	
ILMN_1657968	mitogen-activated protein kinase kinase 2	MAP2K2	1.92E-04	0.025	0.29	-1.31	
ILMN_2160005	nuclear mitotic apparatus protein 1	NUMA1	2.96E-04	0.028	0.29	1.36	
ILMN_1806122	chromodomain helicase DNA binding protein 8	CHD8	9.17E-04	0.036	0.29	-1.19	
ILMN_1757106	membrane-associated ring finger 6	MARCH6		0.049	0.29	1.10	
ILMN_1706553	Smg-7 homolog, nonsense mediated mRNA decay factor (C. elegans), transcript variant 1	SMG7	8.64E-05	0.020	0.30	-1.44	
ILMN_1725992	Rap guanine nucleotide exchange factor (GEF) 6	RAPGEF6	3.11E-04	0.028	0.30	1.13	
ILMN_1771048	PREDICTED: similar to FAM133B protein, transcript variant 1	LOC728153	1.55E-04	0.024	0.30	1.03	
ILMN_1728197	Claudin 5	CLDN5	9.06E-04	0.035	0.30	-1.05	
ILMN_1753467	Sterile alpha motif domain containing 4B	SAMD4B	1.45E-03	0.042	0.31	1.31	
ILMN_1709439	Chromatin modifying protein 1A, transcript variant 2,	CHMP1A	1.73E-04	0.025	0.31	-1.20	
ILMN_1665004	Cancer susceptibility candidate 3	CASC3	1.75E-04	0.025	0.31	1.39	
ILMN_1655990	CDK5 regulatory subunit associated protein 2, transcript variant 1	CDK5RAP2	1.16E-03	0.039	0.32	1.29	
ILMN_1686679	Zinc finger protein 462	ZNF462	4.15E-04	0.030	0.32	1.44	
ILMN_1777982	Upstream transcription factor 1, transcript variant 2,	USF1	2.39E-03	0.050	0.33	1.01	
ILMN_2115949	Zinc finger protein 394	ZNF394	1.09E-03	0.038	0.34	-1.09	
ILMN_2399304	Neuron navigator 2, transcript variant 2,	NAV2	5.92E-04	0.032	0.34	1.27	
ILMN_1768962	A kinase anchor protein 8-like	AKAP8L	4.14E-04	0.030	0.35	1.02	
ILMN_1663042	Syndecan 4	SDC4	3.34E-04	0.029	0.36	-1.00	
ILMN_1655611	Teashirt zinc finger homeobox 2	TSHZ2	2.02E-03	0.047	0.38	-1.04	
ILMN_1696757	Tetratricopeptide repeat domain 14, transcript variant 2,	TTC14	5.92E-04	0.032	0.38	1.02	
ILMN_1682775	Endothelin 1	EDN1	2.50E-04	0.027	0.42	1.26	
ILMN_2078547	Hypothetical protein HSPC268	HSPC268	7.69E-04	0.034	0.42	1.02	
ILMN_1744897	Potassium intermediate/small conductance calcium-activated channel, subfamily N, member 3 , transcript variant 1,	KCNN3	5.09E-04	0.030	0.45	-1.39	

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ILMN_1758067	Regulator of G-protein signalling 4	RGS4	1.04E-03	0.038	-0.47	1.52	Glial
ILMN_2320164	Purinergic receptor P2Y, G-protein coupled 12, transcript variant 1,	P2RY12	8.38E-04	0.035	-0.46	2.49	
ILMN_1703538	Allograft inflammatory factor 1, transcript variant 3,	AIF1	1.43E-03	0.041	-0.29	2.21	
ILMN_1664094	Purinergic receptor P2Y, G-protein coupled 13, transcript variant 1,	P2RY13	5.53E-04	0.031	-0.26	2.07	
ILMN_1674160	Bridging integrator 1, transcript variant 4,	BIN1	2.21E-05	0.019	0.26	1.51	
ILMN_2406299	Sema domain, immunoglobulin domain (Ig), short basic domain, secreted 3B, transcript variant 2,	SEMA3B	3.30E-04	0.029	0.28	3.76	
ILMN_1876924	WNK lysine deficient protein kinase 1	WNK1	6.39E-05	0.020	0.28	1.68	
ILMN_1781636	von Willebrand factor A domain containing 1, transcript variant 1	VWA1	2.68E-04	0.027	0.28	2.96	
ILMN_1684051	WAS protein family, member 2	WASF2	1.16E-05	0.014	0.28	1.92	
ILMN_1704985	Cytochrome P450, family 27, subfamily A, polypeptide 1	CYP27A1	8.62E-04	0.035	0.29	3.24	
ILMN_1811921	Cysteine and glycine-rich protein 1	CSRP1	4.24E-04	0.030	0.29	1.81	
ILMN_1691499	Tight junction protein 1, transcript variant 1	TJP1	2.25E-04	0.027	0.29	1.54	
ILMN_2408039	Eukaryotic translation elongation factor 1 delta, transcript variant 1, mRNA.	EEF1D	1.74E-03	0.045	0.29	1.52	
ILMN_1743103	SH3 and PX domains 2A	SH3PXD2A	3.32E-05	0.020	0.30	1.79	
ILMN_1754660	Chromosome 10 open reading frame 56	C10orf56	1.86E-03	0.046	0.30	1.96	
ILMN_2410938	SPARC related modular calcium binding 1, transcript variant 1,	SMOC1	4.17E-04	0.030	0.31	2.19	
ILMN_1813104	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 2	GALNTL2	6.31E-07	0.008	0.31	3.93	
ILMN_1812262	Discoidin domain receptor tyrosine kinase 1, transcript variant 1	DDR1	1.21E-03	0.039	0.31	2.07	
ILMN_2330382	Progesterone and adipoQ receptor family member VI, transcript variant 2,	PAQR6	1.08E-03	0.038	0.32	2.47	
ILMN_2294123	Septin 4, transcript variant 1,	SEPT4	1.75E-03	0.046	0.33	1.91	
ILMN_2402172	Septin 4, transcript variant 3,	SEPT4	8.25E-04	0.035	0.35	2.45	
ILMN_1665686	Family with sequence similarity 38, member B	FAM38B	2.45E-04	0.027	0.36	5.72	
ILMN_1810420	Dysferlin, limb girdle muscular dystrophy 2B	DYSF	1.75E-03	0.046	0.36	2.95	
ILMN_1670881	Carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 6	CHST6	9.30E-05	0.020	0.36	3.92	
ILMN_1697176	Glial fibrillary acidic protein	GFAP	9.40E-04	0.036	0.37	3.60	

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ILMN_1659895	Moesin	MSN	2.53E-04	0.027	0.37	1.91	Glial
ILMN_1737631	Progesterin and adipoQ receptor family member VI, transcript variant 1	PAQR6	7.85E-04	0.034	0.37	2.47	
ILMN_2323508	Chromosome 9 open reading frame 58, transcript variant 2	C9orf58	2.20E-03	0.048	0.38	2.25	
ILMN_1752668	Dishevelled associated activator of morphogenesis 2	DAAM2	3.78E-04	0.029	0.42	2.25	
ILMN_1750271	Myelin-associated oligodendrocyte basic protein	MOBP	4.33E-04	0.030	0.51	2.46	
ILMN_2331544	Myelin basic protein transcript variant 7	MBP	6.95E-04	0.033	0.64	2.55	
ILMN_1851540	AV707343 ADB cDNA clone ADBB5H02 5,		9.12E-04	0.036	-0.31	ND	ND
ILMN_1850027	CR742772		5.97E-04	0.032	-0.27	ND	ND
ILMN_1828967	cDNA FLJ12023 fis, clone HEMBB1001785		7.59E-04	0.034	0.26	ND	ND
ILMN_1867517	cDNA FLJ31407 fis, clone NT2NE2000137		1.21E-03	0.039	0.30	ND	ND
ILMN_1903914	cDNA FLJ26188 fis, clone ADG04821		3.40E-04	0.029	0.38	ND	ND
ILMN_1912737	mRNA; cDNA DKFZp686F1546 (from clone DKFZp686F1546)		4.73E-06	0.012	0.41	ND	ND